

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/079,785

1646

#3
7/29/98
msDATE: 07/27/98
TIME: 16:33:46

INPUT SET: S3265.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Goodwin, Raymond G.
Smith, Craig A.
Armitage, Richard J.
Gruss, Hans-Jurgen

(ii) TITLE OF INVENTION: Novel Cytokine That Binds CD30

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kathryn A. Seese, Immunex Corporation
(B) STREET: 51 University Street
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Apple 7.1
(D) SOFTWARE: Microsoft Word, Version 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/079,785
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/225,989
(B) FILING DATE: 12 APRIL 1994

(A) APPLICATION NUMBER: US 07/966,775
(B) FILING DATE: 27-OCT-1992
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 907,224
(B) FILING DATE: 01-JUL-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 899,660

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/079,785DATE: 07/27/98
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47 (B) FILING DATE: 15-JUN-1992
48
49 (vii) PRIOR APPLICATION DATA:
50 (A) APPLICATION NUMBER: US 892,459
51 (B) FILING DATE: 02-JUN-1992
52
53 (vii) PRIOR APPLICATION DATA:
54 (A) APPLICATION NUMBER: US 889,717
55 (B) FILING DATE: 26-MAY-1992
56
57 (viii) ATTORNEY/AGENT INFORMATION:
58 (A) NAME: Seese, Kathryn A.
59 (B) REGISTRATION NUMBER: 32,172
60 (C) REFERENCE/DOCKET NUMBER: 2804-E
61
62 (ix) TELECOMMUNICATION INFORMATION:
63 (A) TELEPHONE: (206)587-0430
64 (B) TELEFAX: (206)233-0644
65 (C) TELEX: 756822
66
67
68 (2) INFORMATION FOR SEQ ID NO:1:
69
70 (i) SEQUENCE CHARACTERISTICS:
71 (A) LENGTH: 1788 base pairs
72 (B) TYPE: nucleic acid
73 (C) STRANDEDNESS: single
74 (D) TOPOLOGY: linear
75
76 (ii) MOLECULE TYPE: cDNA to mRNA
77
78 (iii) HYPOTHETICAL: NO
79
80 (iv) ANTI-SENSE: NO
81
82
83 (vii) IMMEDIATE SOURCE:
84 (B) CLONE: huCD30
85
86 (ix) FEATURE:
87 (A) NAME/KEY: CDS
88 (B) LOCATION: 1..1788
89
90
91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
92
93 ATG CGC GTC CTC CTC GCC GCG CTG GGA CTG CTG TTC CTG GGG GCG CTA 48
94 Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
95 1 5 10 15
96
97 CGA GCC TTC CCA CAG GAT CGA CCC TTC GAG GAC ACC TGT CAT GGA AAC 96
98 Arg Ala Phe Pro Gln Asp Arg Pro Phe Glu Asp Thr Cys His Gly Asn
99 20 25 30

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100																		
101	CCC	AGC	CAC	TAC	TAT	GAC	AAG	GCT	GTC	AGG	AGG	TGC	TGT	TAC	CGC	TGC	144	
102	Pro	Ser	His	Tyr	Tyr	Asp	Lys	Ala	Val	Arg	Arg	Cys	Cys	Tyr	Arg	Cys		
103			35					40					45					
104																		
105	CCC	ATG	GGG	CTG	TTC	CCG	ACA	CAG	CAG	TGC	CCA	CAG	AGG	CCT	ACT	GAC	192	
106	Pro	Met	Gly	Leu	Phe	Pro	Thr	Gln	Gln	Cys	Pro	Gln	Arg	Pro	Thr	Asp		
107		50					55					60						
108																		
109	TGC	AGG	AAG	CAG	TGT	GAG	CCT	GAC	TAC	TAC	CTG	GAT	GAG	GCC	GAC	CGC	240	
110	Cys	Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Asp	Arg		
111	65					70					75					80		
112																		
113	TGT	ACA	GCC	TGC	GTG	ACT	TGT	TCT	CGA	GAT	GAC	CTC	GTG	GAG	AAG	ACG	288	
114	Cys	Thr	Ala	Cys	Val	Thr	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr		
115					85				90						95			
116																		
117	CCG	TGT	GCA	TGG	AAC	TCC	TCC	CGT	GTC	TGC	GAA	TGT	CGA	CCC	GGC	ATG	336	
118	Pro	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Val	Cys	Glu	Cys	Arg	Pro	Gly	Met		
119				100					105					110				
120																		
121	TTC	TGT	TCC	ACG	TCT	GCC	GTC	AAC	TCC	TGT	GCC	CGC	TGC	TTC	TTC	CAT	384	
122	Phe	Cys	Ser	Thr	Ser	Ala	Val	Asn	Ser	Cys	Ala	Arg	Cys	Phe	Phe	His		
123			115					120					125					
124																		
125	TCT	GTC	TGT	CCG	GCA	GGG	ATG	ATT	GTC	AAG	TTC	CCA	GGC	ACG	GCG	CAG	432	
126	Ser	Val	Cys	Pro	Ala	Gly	Met	Ile	Val	Lys	Phe	Pro	Gly	Thr	Ala	Gln		
127		130					135					140						
128																		
129	AAG	AAC	ACG	GTC	TGT	GAG	CCG	GCT	TCC	CCA	GGG	GTC	AGC	CCT	GCC	TGT	480	
130	Lys	Asn	Thr	Val	Cys	Glu	Pro	Ala	Ser	Pro	Gly	Val	Ser	Pro	Ala	Cys		
131	145					150					155					160		
132																		
133	GCC	AGC	CCA	GAG	AAC	TGC	AAG	GAA	CCC	TCC	AGT	GGC	ACC	ATC	CCC	CAG	528	
134	Ala	Ser	Pro	Glu	Asn	Cys	Lys	Glu	Pro	Ser	Ser	Gly	Thr	Ile	Pro	Gln		
135					165				170						175			
136																		
137	GCC	AAG	CCC	ACC	CCG	GTG	TCC	CCA	GCA	ACC	TCC	AGT	GCC	AGC	ACC	ATG	576	
138	Ala	Lys	Pro	Thr	Pro	Val	Ser	Pro	Ala	Thr	Ser	Ser	Ala	Ser	Thr	Met		
139				180					185					190				
140				</														

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153	AGA	AAG	CAG	TGT	GAG	CCC	GAC	TAC	TAC	CTG	GAC	GAG	GCC	GGC	CGC	TGC	768
154	Arg	Lys	Gln	Cys	Glu	Pro	Asp	Tyr	Tyr	Leu	Asp	Glu	Ala	Gly	Arg	Cys	
155					245					250					255		
156																	
157	ACA	GCC	TGC	GTG	AGC	TGT	TCT	CGA	GAT	GAC	CTT	GTG	GAG	AAG	ACG	CCA	816
158	Thr	Ala	Cys	Val	Ser	Cys	Ser	Arg	Asp	Asp	Leu	Val	Glu	Lys	Thr	Pro	
159				260					265					270			
160																	
161	TGT	GCA	TGG	AAC	TCC	TCC	CGC	ACC	TGC	GAA	TGT	CGA	CCT	GGC	ATG	ATC	864
162	Cys	Ala	Trp	Asn	Ser	Ser	Arg	Thr	Cys	Glu	Cys	Arg	Pro	Gly	Met	Ile	
163			275					280					285				
164																	
165	TGT	GCC	ACA	TCA	GCC	ACC	AAC	TCC	TGT	GCC	CGC	TGT	GTC	CCC	TAC	CCA	912
166	Cys	Ala	Thr	Ser	Ala	Thr	Asn	Ser	Cys	Ala	Arg	Cys	Val	Pro	Tyr	Pro	
167		290					295					300					
168																	
169	ATC	TGT	GCA	GGA	GAG	ACG	GTC	ACC	AAG	CCC	CAG	GAT	ATG	GCT	GAG	AAG	960
170	Ile	Cys	Ala	Gly	Glu	Thr	Val	Thr	Lys	Pro	Gln	Asp	Met	Ala	Glu	Lys	
171	305					310					315					320	
172																	
173	GAC	ACC	ACC	TTT	GAG	GCG	CCA	CCC	CTG	GGG	ACC	CAG	CCG	GAC	TGC	AAC	1008
174	Asp	Thr	Thr	Phe	Glu	Ala	Pro	Pro	Leu	Gly	Thr	Gln	Pro	Asp	Cys	Asn	
175				325						330					335		
176																	
177	CCC	ACC	CCA	GAG	AAT	GGC	GAG	GCG	CCT	GCC	AGC	ACC	AGC	CCC	ACT	CAG	1056
178	Pro	Thr	Pro	Glu	Asn	Gly	Glu	Ala	Pro	Ala	Ser	Thr	Ser	Pro	Thr	Gln	
179			340						345					350			
180																	
181	AGC	TTG	CTG	GTG	GAC	TCC	CAG	GCC	AGT	AAG	ACG	CTG	CCC	ATC	CCA	ACC	1104
182	Ser	Leu	Leu	Val	Asp	Ser	Gln	Ala	Ser	Lys	Thr	Leu	Pro	Ile	Pro	Thr	
183			355					360					365				
184																	
185	AGC	GCT	CCC	GTC	GCT	CTC	TCC	TCC	ACG	GGG	AAG	CCC	GTT	CTG	GAT	GCA	1152
186	Ser	Ala	Pro	Val	Ala	Leu	Ser	Ser	Thr	Gly	Lys	Pro	Val	Leu	Asp	Ala	
187		370					375					380					
188																	
189	GGG	CCA	GTG	CTC	TTC	TGG	GTG	ATC	CTG	GTG	TTG	GTT	GTG	GTG	GTC	GGC	1200
190	Gly	Pro	Val	Leu	Phe	Trp	Val	Ile	Leu	Val	Leu	Val	Val	Val	Val	Gly	
191	385					390					395					400	
192																	
193	TCC	AGC	GCC	TTC	CTC	CTG	TGC	CAC	CGG	AGG	GCC	TGC	AGG	AAG	CGA	ATT	1248
194	Ser	Ser	Ala	Phe	Leu	Leu	Cys	His	Arg	Arg	Ala	Cys	Arg	Lys	Arg	Ile	
195				405						410					415		
196																	
197	CGG	CAG	AAG	CTC	CAC	CTG	TGC	TAC	CCG	GTC	CAG	ACC	TCC	CAG	CCC	AAG	1296
198	Arg	Gln	Lys	Leu	His	Leu	Cys	Tyr	Pro	Val	Gln	Thr	Ser	Gln	Pro	Lys	
199			420						425					430			
200																	
201	CTA	GAG	CTT	GTG	GAT	TCC	AGA	CCC	AGG	AGG	AGC	TCA	ACG	CAG	CTG	AGG	1344
202	Leu	Glu	Leu	Val	Asp	Ser	Arg	Pro	Arg	Arg	Ser	Ser	Thr	Gln	Leu	Arg	
203			435					440					445				
204																	
205	AGT	GGT	GCG	TCG	GTG	ACA	GAA	CCC	GTC	GCG	GAA	GAG	CGA	GGG	TTA	ATG	1392

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206 Ser Gly Ala Ser Val Thr Glu Pro Val Ala Glu Glu Arg Gly Leu Met
207      450                      455                      460
208
209 AGC CAG CCA CTG ATG GAG ACC TGC CAC AGC GTG GGG GCA GCC TAC CTG 1440
210 Ser Gln Pro Leu Met Glu Thr Cys His Ser Val Gly Ala Ala Tyr Leu
211 465                      470                      475                      480
212
213 GAG AGC CTG CCG CTG CAG GAT GCC AGC CCG GCC GGG GGC CCC TCG TCC 1488
214 Glu Ser Leu Pro Leu Gln Asp Ala Ser Pro Ala Gly Gly Pro Ser Ser
215                      485                      490                      495
216
217 CCC AGG GAC CTT CCT GAG CCC CGG GTG TCC ACG GAG CAC ACC AAT AAC 1536
218 Pro Arg Asp Leu Pro Glu Pro Arg Val Ser Thr Glu His Thr Asn Asn
219      500                      505                      510
220
221 AAG ATT GAG AAA ATC TAC ATC ATG AAG GCT GAC ACC GTG ATC GTG GGG 1584
222 Lys Ile Glu Lys Ile Tyr Ile Met Lys Ala Asp Thr Val Ile Val Gly
223      515                      520                      525
224
225 ACC GTG AAG GCT GAG CTG CCG GAG GGC CGG GGC CTG GCG GGG CCA GCA 1632
226 Thr Val Lys Ala Glu Leu Pro Glu Gly Arg Gly Leu Ala Gly Pro Ala
227      530                      535                      540
228
229 GAG CCC GAG TTG GAG GAG GAG CTG GAG GCG GAC CAT ACC CCC CAC TAC 1680
230 Glu Pro Glu Leu Glu Glu Glu Leu Glu Ala Asp His Thr Pro His Tyr
231 545                      550                      555                      560
232
233 CCC GAG CAG GAG ACA GAA CCG CCT CTG GGC AGC TGC AGC GAT GTC ATG 1728
234 Pro Glu Gln Glu Thr Glu Pro Pro Leu Gly Ser Cys Ser Asp Val Met
235                      565                      570                      575
236
237 CTC TCA GTG GAA GAG GAA GGG AAA GAA GAC CCC TTG CCC ACA GCT GCC 1776
238 Leu Ser Val Glu Glu Glu Gly Lys Glu Asp Pro Leu Pro Thr Ala Ala
239      580                      585                      590
240
241 TCT GGA AAG TGA 1788
242 Ser Gly Lys
243      595
244
245
246 (2) INFORMATION FOR SEQ ID NO:2:
247
248 (i) SEQUENCE CHARACTERISTICS:
249 (A) LENGTH: 595 amino acids
250 (B) TYPE: amino acid
251 (D) TOPOLOGY: linear
252
253 (ii) MOLECULE TYPE: protein
254
255 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
256
257 Met Arg Val Leu Leu Ala Ala Leu Gly Leu Leu Phe Leu Gly Ala Leu
258 1 5 10 15

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/079,785

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Line	Error	Original Text
39	Wrong Classification	(C) CLASSIFICATION:435